



BLAST2 Search Results

EXHIBIT A

Docket No.: PF-0609 USN
USN: 09/806,267

Sequences

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GCG Assembly

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BLAST2 Manual

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Program: blastp

Sequence ID(s):

☐ 1859631CD1 vs. genpept137

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 1859631CD1
(254 letters)

Database: genpept137
1,534,369 sequences; 474,463,515 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
<input checked="" type="checkbox"/> <u>g6807669</u> hypothetical protein [Homo sapiens]	520	e-146
<input checked="" type="checkbox"/> <u>g5731207</u> CRIB-containing BORG2 protein [Homo sapiens]	520	e-146
<input checked="" type="checkbox"/> <u>g30585393</u> Homo sapiens CDC42 effector protein (Rho GTPase bin	520	e-146
<input checked="" type="checkbox"/> <u>g30583219</u> CDC42 effector protein (Rho GTPase binding) 3 [Homo	520	e-146
<input checked="" type="checkbox"/> <u>g17939543</u> Unknown (protein for MGC:3481) [Homo sapiens]	520	e-146
<input checked="" type="checkbox"/> <u>g3834633</u> MSE55-related protein [Homo sapiens]	518	e-146
<input checked="" type="checkbox"/> <u>g4324454</u> Cdc42 effector protein 3 [Homo sapiens]	518	e-146
<input checked="" type="checkbox"/> <u>g21961178</u> CDC42 effector protein (Rho GTPase binding) 3 [Mus	483	e-135
<input checked="" type="checkbox"/> <u>g18204088</u> CDC42 effector protein (Rho GTPase binding) 3 [Mus	483	e-135
<input checked="" type="checkbox"/> <u>g12859655</u> unnamed protein product [Mus musculus]	483	e-135

>g6807669 hypothetical protein [Homo sapiens]
Length = 254

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60

Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60

Query: 61 GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Sbjct: 61 GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVLNVMMDKNK 254
SLLDEVLNVMMDKNK

Sbjct: 241 SLLDEVLNVMMDKNK 254

>g5731207 CRIB-containing BORG2 protein [Homo sapiens]
Length = 254

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60

Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60

Query: 61 GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Sbjct: 61 GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVLNVMMDKNK 254
SLLDEVLNVMMDKNK

Sbjct: 241 SLLDEVLNVMMDKNK 254

>g30585393 Homo sapiens CDC42 effector protein (Rho GTPase binding)
3 [synthetic construct]
Length = 255

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60

Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDFVFGDISFLQ 60

Query: 61 GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Sbjct: 61 GNYELLPGNQEKAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNMDKNK 254
SLLDEVNLNMDKNK
Sbjct: 241 SLLDEVNLNMDKNK 254

>g30583219 CDC42 effector protein (Rho GTPase binding) 3 [Homo sapiens]
Length = 254

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61 GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEEKAEKSSLENGTVHQDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEEKAEKSSLENGTVHQDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEEKAEKSSLENGTVHQDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNMDKNK 254
SLLDEVNLNMDKNK
Sbjct: 241 SLLDEVNLNMDKNK 254

>g17939543 Unknown (protein for MGC:3481) [Homo sapiens]
Length = 254

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61 GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEEKAEKSSLENGTVHQDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEEKAEKSSLENGTVHQDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEEKAEKSSLENGTVHQDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNMDKNK 254
SLLDEVNLNMDKNK
Sbjct: 241 SLLDEVNLNMDKNK 254

>g3834633 MSE55-related protein [Homo sapiens]
Length = 254

Score = 518 bits (1320), Expect = e-146
Identities = 253/254 (99%), Positives = 253/254 (99%)

```
Query: 1  MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
          MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1  MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61  GNYELLPGNQEKALHGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
          GNYELLPGNQEKALHGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61  GNYELLPGNQEKALHGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121  PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
          PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121  PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181  SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP 240
          SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP
Sbjct: 181  SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP 240

Query: 241  SLLDEVLNVMMDKNK 254
          SLLDEVLNVMMDKNK
Sbjct: 241  SLLDEVLNVMMDKNK 254
```

>g4324454 Cdc42 effector protein 3 [Homo sapiens]
Length = 254

Score = 518 bits (1319), Expect = e-146
Identities = 253/254 (99%), Positives = 253/254 (99%)

```
Query: 1  MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
          MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGD SFLQ
Sbjct: 1  MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDNSFLQ 60

Query: 61  GNYELLPGNQEKALHGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
          GNYELLPGNQEKALHGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61  GNYELLPGNQEKALHGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121  PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
          PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121  PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181  SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP 240
          SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP
Sbjct: 181  SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP 240

Query: 241  SLLDEVLNVMMDKNK 254
          SLLDEVLNVMMDKNK
Sbjct: 241  SLLDEVLNVMMDKNK 254
```

>g21961178 CDC42 effector protein (Rho GTPase binding) 3 [Mus musculus]
Length = 254

Score = 483 bits (1230), Expect = e-135
Identities = 235/254 (92%), Positives = 242/254 (94%)

```
Query: 1  MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
          MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1  MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
```

Query: 61 GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEK AH QFPGHN+FFRANSTSDS+FTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEK AHSQFPGHNDFFRANSTSDSMFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTF+SKQESFG KLPRLSCEPVMEEK QE+SSLLENG VHQGDTSWGSSGS SQ
Sbjct: 121 PLLSPVTFHSKQESFGRPKLRLSCEPVMEEKVQEQQSSLLENGAVHQGDTSWGSSGSQSQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQ DWPA+DMF+HP CEL+K KTKSEES SDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQSSDWPADDMFEHPASCELVKSKTKSEESFSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNMDKNK 254
SLLDEVNLNMDKNK
Sbjct: 241 SLLDEVNLNMDKNK 254

>g18204088 CDC42 effector protein (Rho GTPase binding) 3 [Mus musculus]
Length = 254

Score = 483 bits (1230), Expect = e-135
Identities = 235/254 (92%), Positives = 242/254 (94%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61 GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEK AH QFPGHN+FFRANSTSDS+FTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEK AHSQFPGHNDFFRANSTSDSMFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTF+SKQESFG KLPRLSCEPVMEEK QE+SSLLENG VHQGDTSWGSSGS SQ
Sbjct: 121 PLLSPVTFHSKQESFGRPKLRLSCEPVMEEKVQEQQSSLLENGAVHQGDTSWGSSGSQSQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQ DWPA+DMF+HP CEL+K KTKSEES SDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQSSDWPADDMFEHPASCELVKSKTKSEESFSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNMDKNK 254
SLLDEVNLNMDKNK
Sbjct: 241 SLLDEVNLNMDKNK 254

>g12859655 unnamed protein product [Mus musculus]
Length = 254

Score = 483 bits (1230), Expect = e-135
Identities = 235/254 (92%), Positives = 242/254 (94%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61 GNYELLPGNQEK AHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEK AH QFPGHN+FFRANSTSDS+FTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEK AHSQFPGHNDFFRANSTSDSMFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLRLSCEPVMEEKAQEKSSLLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTF+SKQESFG KLPRLSCEPVMEEK QE+SSLLENG VHQGDTSWGSSGS SQ
Sbjct: 121 PLLSPVTFHSKQESFGRPKLRLSCEPVMEEKVQEQQSSLLENGAVHQGDTSWGSSGSQSQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQ DWPA+DMF+HP CEL+K KTKSEES SDLTGSLLSLQLDLGP

Sbjct: 181 SSQGRDSHSSSLSEQSSDWPADDMFEHPASCELVKSKTKSEESFSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNVMKKNK 254
SLLDEVNLNVMKKNK

Sbjct: 241 SLLDEVNLNVMKKNK 254

Database: genpept137

Posted date: Sep 11, 2003 11:22 AM

Number of letters in database: 474,463,515

Number of sequences in database: 1,534,369

Lambda	K	H
0.311	0.131	0.377

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 250360315

Number of Sequences: 1534369

Number of extensions: 10716561

Number of successful extensions: 21567

Number of sequences better than 10.0: 99

Number of HSP's better than 10.0 without gapping: 53

Number of HSP's successfully gapped in prelim test: 46

Number of HSP's that attempted gapping in prelim test: 21369

Number of HSP's gapped (non-prelim): 184

length of query: 254

length of database: 474,463,515

effective HSP length: 60

effective length of query: 194

effective length of database: 382,401,375

effective search space: 74185866750

effective search space used: 74185866750

T: 11

A: 40

X1: 16 (7.2 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 42 (21.8 bits)

Graphical Viewer...

Submit sequences to: BLAST2



Submit

Reset

